

WHAT IS CLAIMED IS:

1. An isolated nucleic acid comprising a mutant DNA encoding a *Candida rugosa* lipase, wherein the mutant DNA is at least 80% identical to a wild-type DNA encoding the *Candida rugosa* lipase, and includes at least 12 codons corresponding to CTG codons in the wild-type DNA, each of the 12 codons, independently, being TCT, TCC, TCA, TCG, AGT, or AGC.

2. The nucleic acid of claim 1, wherein at least 15 codons correspond to CTG codons in the wild-type DNA, each of the 15 codons, independently, being TCT, TCC, TCA, TCG, AGT, or AGC.

3. The nucleic acid of claim 2, wherein the amino acid sequence of the *Candida rugosa* lipase is at least 90% identical to SEQ ID NO:2, 4, 6, 8, or 10.

4. The nucleic acid of claim 2, wherein all codons correspond to CTG codons in the wild-type DNA, each of the codons, independently, being TCT, TCC, TCA, TCG, AGT, or AGC.

5. The nucleic acid of claim 4, wherein the amino acid sequence of the *Candida rugosa* lipase is at least 90% identical to SEQ ID NO:2, 4, 6, 8, or 10.

6. The nucleic acid of claim 5, wherein the amino acid sequence of the *Candida rugosa* lipase is SEQ ID NO:2, 4, 6, 8, or 10.

7. The nucleic acid of claim 1, wherein the mutant DNA is at least 85% identical to a wild-type DNA encoding the *Candida rugosa* lipase.

8. The nucleic acid of claim 7, wherein at least 15 codons correspond to CTG codons in the wild-type DNA, each of the 15 codons, independently, being TCT, TCC, TCA, TCG, AGT, or AGC.

1 9. The nucleic acid of claim 8, wherein the amino acid sequence of the *Candida*
2 *rugosa* lipase is at least 90% identical to SEQ ID NO:2, 4, 6, 8, or 10.

1 10. The nucleic acid of claim 8, wherein all codons correspond to CTG codons in
2 the wild-type DNA, each of the codons, independently, being TCT, TCC, TCA, TCG, AGT,
3 or AGC.

1 11. The nucleic acid of claim 10, wherein the amino acid sequence of the *Candida*
2 *rugosa* lipase is at least 90% identical to SEQ ID NO:2, 4, 6, 8, or 10.

1 12. The nucleic acid of claim 11, wherein the amino acid sequence of the *Candida*
2 *rugosa* lipase is SEQ ID NO:2, 4, 6, 8, or 10.

1 13. The nucleic acid of claim 1, wherein the mutant DNA is at least 90% identical
2 to a wild-type DNA encoding the *Candida rugosa* lipase.

1 14. The nucleic acid of claim 13, wherein at least 15 codons correspond to CTG
2 codons in the wild-type DNA, each of the 15 codons, independently, being TCT, TCC, TCA,
3 TCG, AGT, or AGC.

1 15. The nucleic acid of claim 14, wherein the amino acid sequence of the *Candida*
2 *rugosa* lipase is at least 90% identical to SEQ ID NO:2, 4, 6, 8, or 10.

1 16. The nucleic acid of claim 14, wherein all codons correspond to CTG codons
2 in the wild-type DNA, each of the codons, independently, being TCT, TCC, TCA, TCG,
3 AGT, or AGC.

1 17. The nucleic acid of claim 16, wherein the amino acid sequence of the *Candida*
2 *rugosa* lipase is at least 90% identical to SEQ ID NO:2, 4, 6, 8, or 10.

1 18. The nucleic acid of claim 17, wherein the amino acid sequence of the *Candida*
2 *rugosa* lipase is SEQ ID NO:2, 4, 6, 8, or 10.

1 19. A microorganism comprising the nucleic acid of claim 1, wherein the
2 microorganism is a bacterium.

1 20. The microorganism of claim 19, wherein the bacterium is *E. coli*.

1 21. The microorganism of claim 19, wherein the mutant DNA is at least 85%
2 identical to a wild-type DNA encoding the *Candida rugosa* lipase.

1 22. The microorganism of claim 21, wherein the bacterium is *E. coli*.

1 23. The microorganism of claim 19, wherein the mutant DNA is at least 90%
2 identical to a wild-type DNA encoding the *Candida rugosa* lipase.

1 24. The microorganism of claim 23, wherein the bacterium is *E. coli*.

1 25. An isolated nucleic acid, comprising a DNA of SEQ ID NO:1, 3, 5, 7, or 9; or
2 a degenerate variant thereof.

1 26. A method for preparing a mutant DNA encoding a *Candida rugosa* lipase,
2 comprising:
3 providing a wild-type DNA encoding a *Candida rugosa* lipase; and
4 conducting PCR amplification by mixing the wild-type DNA, a DNA polymerase, a
5 pair of external primers encompassing the entirety of the wild-type DNA, and a number of
6 pairs of internal primers respectively encompassing fragments of the wild-type DNA,
7 wherein each of the internal primers includes one or more of universal codons and anticodons
8 for serine selected from TCT, TCC, TCA, TCG, AGT, AGC, AGA, GGA, TGA, CGA, ACT,
9 and GCT, in which the universal codons and anitcodons correspond to at least 12 CTG
10 codons in the wild-type DNA; and each internal primer overlaps with another internal or
11 external primer in a manner that a mutant DNA encoding the *Candida rugosa* lipase is
12 obtained.

1 27. The method of claim 26, wherein at least 15 codons correspond to CTG
2 codons in the wild-type DNA, each of the 15 codons, independently, being TCT, TCC, TCA,
3 TCG, AGT, or AGC.

1 28. The method of claim 27, wherein the amino acid sequence of the *Candida*
2 *rugosa* lipase is at least 90% identical to SEQ ID NO:2, 4, 6, 8, or 10.

1 29. The method of claim 27, wherein all codons correspond to CTG codons in the
2 wild-type DNA, each of the codons, independently, being TCT, TCC, TCA, TCG, AGT, or
3 AGC.

1 30. The method of claim 29, wherein the amino acid sequence of the *Candida*
2 *rugosa* lipase is at least 90% identical to SEQ ID NO:2, 4, 6, 8, or 10.

1 31. The method of claim 30, wherein the amino acid sequence of the *Candida*
2 *rugosa* lipase is SEQ ID NO:2, 4, 6, 8, or 10.

1 32. The method of claim 26, wherein the mutant DNA is SEQ ID NO:1, 3, 5, 7, or
2 9; or a degenerate variant thereof.

1 33. A chimeric *Candida rugosa* lipase comprising a substrate interacting domain
2 of a first *Candida rugosa* lipase and a non-substrate interacting domain of a second *Candida*
3 *rugosa* lipase.

1 34. The lipase of claim 33, wherein the second *Candida rugosa* lipase is SEQ ID
2 NO:6.

1 35. The lipase of claim 33, wherein the first *Candida rugosa* lipase is SEQ ID
2 NO:2, 4, 8, or 10.